RAW SEQUENCE LISTING   DATE: 05/03/2001
PATENT APPLICATION: US/09/828,739   TIME: 11:57:22

Input Set : N:\Crf3\RULE60\09828739.txt
Output Set: N:\CRF3\05032001\I828739.raw

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 3 <110> APPLICANT: Ashkenazi, Avi J.
 4        Chuntharapai, Anan
 5        Kim, K. Jin
 7 <120> TITLE OF INVENTION: METHOD FOR MAKING MONOCLONAL ANTIBODIES AND
 8        CROSS-REACTIVE ANTIBODIES OBTAINABLE BY THE METHOD
10 <130> FILE REFERENCE: P1468R1 (REVISED)
12 <140> CURRENT APPLICATION NUMBER: 09/828,739
13 <141> CURRENT FILING DATE: 2001-04-09
15 <150> PRIOR APPLICATION NUMBER: US 09/329,633
16 <151> PRIOR FILING DATE: 1999-06-10
18 <150> PRIOR APPLICATION NUMBER: US 60/089,253
19 <151> PRIOR FILING DATE: 1998-06-12
21 <160> NUMBER OF SEQ ID NOS: 2
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 1799
25 <212> TYPE: DNA
26 <213> ORGANISM: human
28 <400> SEQUENCE: 1
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31  gcgcccacaa aatacaccga cgatgcccga tctactttaa gggctgaaac 100
33  ccacgggcct gagagactat aagagcgttc cctaccgcca tggaacaacg 150
35  gggacagaac gccccggccg cttcgggggc ccggaaaagg cacggcccag 200
37  gacccaggga ggcgcgggga gccaggcctg ggctccgggt ccccaagacc 250
39  cttgtgctcg ttgtcgccgc ggtcctgctg ttggtctcag ctgagtctgc 300
41  tctgatcacc caacaagacc tagctcccca gcagagagcg gccccacaac 350
43  aaaagaggtc cagcccctca gagggattgt gtccacctgg acaccatatc 400
45  tcagaagacg gtagagattg catctcctgc aaatatggac aggactatag 450
47  cactcactgg aatgacctcc ttttctgctt gcgctgcacc aggtgtgatt 500
49  caggtgaagt ggagctaagt ccctgcacca cgaccagaaa cacagtgtgt 550
51  cagtgcgaag aaggcacctt ccgggaagaa gattctcctg agatgtgccg 600
53  gaagtgccgc acagggtgtc ccagagggat ggtcaaggtc ggtgattgta 650
55  caccctggag tgacatcgaa tgtgtccaca agaatcagg catcatcata 700
57  ggagtcacag ttgcagccgt agtcttgatt gtggctgtgt ttgtttgcaa 750
59  gtctttactg tggaagaaag tccttcctta cctgaaaggc atctgctcag 800
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63  gctgaggaca atgtcctcaa tgagatcgtg agtatcttgc agcccaccca 900
65  ggtccctgag caggaaatgg aagtccagga gccagcagag ccaacaggtg 950
67  tcaacatgtt gtcccccggg gagtcagagc atctgctgga accggcagaa 1000
69  gctgaaaggt ctcagaggag gaggctgctg gttccagcaa atgaaggtga 1050
71  tcccactgag actctgagac agtgcttcga tgactttgca gacttggtgc 1100
73  cctttgactc ctgggagccg ctcatgagga agttgggcct catggacaat 1150
75  gagataaagg tggctaaagc tgaggcagcg ggccacaggg acaccttgta 1200
77  cacgatgctg ataaagtggg tcaacaaaac cgggcgagat gcctctgtcc 1250
79  acaccctgct ggatgccttg gagacgctgg gagagagact tgccaagcag 1300
81  aagattgagg accacttgtt gagctctgga aagttcatgt atctagaagg 1350
83  taatgcagac tctgccwtgt cctaagtgtg attctcttca ggaagtgaga 1400
85  ccttccctgg tttacctttt ttctggaaaa agcccaactg gactccagtc 1450
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 87  agtaggaaag tgccacaatt gtcacatgac cggtactgga agaaactctc 1500
 89  ccatccaaca tcacccagtg gatggaacat cctgtaactt ttcactgcac 1550
 91  ttggcattat ttttataagc tgaatgtgat aataaggaca ctatggaaat 1600
 93  gtctggatca ttccgtttgt gcgtactttg agatttggtt tgggatgtca 1650
 95  ttgttttcac agcacttttt tatcctaatg taaatgcttt atttatttat 1700
 97  ttgggctaca ttgtaagatc catctacaaa aaaaaaaaaa aaaaaaaaag 1750
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102  <211> LENGTH: 411
103  <212> TYPE: PRT
104  <213> ORGANISM: human
106  <220> FEATURE:
107  <221> NAME/KEY: xaa
108  <222> LOCATION: 410
109  <223> OTHER INFORMATION: xaa = leu or met
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112  Met Glu Gln Arg Gly Gln Asn Ala Pro Ala Ala Ser Gly Ala Arg
113   1               5                  10                  15
115  Lys Arg His Gly Pro Gly Pro Arg Glu Ala Arg Gly Ala Arg Pro
116                  20                  25                  30
118  Gly Leu Arg Val Pro Lys Thr Leu Val Leu Val Val Ala Ala Val
119                  35                  40                  45
121  Leu Leu Leu Val Ser Ala Glu Ser Ala Leu Ile Thr Gln Gln Asp
122                  50                  55                  60
124  Leu Ala Pro Gln Gln Arg Ala Ala Pro Gln Gln Lys Arg Ser Ser
125                  65                  70                  75
127  Pro Ser Glu Gly Leu Cys Pro Pro Gly His His Ile Ser Glu Asp
128                  80                  85                  90
130  Gly Arg Asp Cys Ile Ser Cys Lys Tyr Gly Gln Asp Tyr Ser Thr
131                  95                 100                 105
133  His Trp Asn Asp Leu Leu Phe Cys Leu Arg Cys Thr Arg Cys Asp
134                 110                 115                 120
136  Ser Gly Glu Val Glu Leu Ser Pro Cys Thr Thr Thr Arg Asn Thr
137                 125                 130                 135
139  Val Cys Gln Cys Glu Glu Gly Thr Phe Arg Glu Glu Asp Ser Pro
140                 140                 145                 150
142  Glu Met Cys Arg Lys Cys Arg Thr Gly Cys Pro Arg Gly Met Val
143                 155                 160                 165
145  Lys Val Gly Asp Cys Thr Pro Trp Ser Asp Ile Glu Cys Val His
146                 170                 175                 180
148  Lys Glu Ser Gly Ile Ile Ile Gly Val Thr Val Ala Ala Val Val
149                 185                 190                 195
151  Leu Ile Val Ala Val Phe Val Cys Lys Ser Leu Leu Trp Lys Lys
152                 200                 205                 210
154  Val Leu Pro Tyr Leu Lys Gly Ile Cys Ser Gly Gly Gly Gly Asp
155                 215                 220                 225
157  Pro Glu Arg Val Asp Arg Ser Ser Gln Arg Pro Gly Ala Glu Asp
158                 230                 235                 240
160  Asn Val Leu Asn Glu Ile Val Ser Ile Leu Gln Pro Thr Gln Val
```

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  161                245             250                255
  163  Pro Glu Gln Glu Met Glu Val Gln Glu Pro Ala Glu Pro Thr Gly
  164                260             265                270
  166  Val Asn Met Leu Ser Pro Gly Glu Ser Glu His Leu Leu Glu Pro
  167                275             280                285
  169  Ala Glu Ala Glu Arg Ser Gln Arg Arg Arg Leu Leu Val Pro Ala
  170                290             295                300
  172  Asn Glu Gly Asp Pro Thr Glu Thr Leu Arg Gln Cys Phe Asp Asp
  173                305             310 ,              315
  175  Phe Ala Asp Leu Val Pro Phe Asp Ser Trp Glu Pro Leu Met Arg
  176                320             325                330
  178  Lys Leu Gly Leu Met Asp Asn Glu Ile Lys Val Ala Lys Ala Glu
  179                335             340                345
  181  Ala Ala Gly His Arg Asp Thr Leu Tyr Thr Met Leu Ile Lys Trp
  182                350             355                360
  184  Val Asn Lys Thr Gly Arg Asp Ala Ser Val His Thr Leu Leu Asp
  185                365             370                375
  187  Ala Leu Glu Thr Leu Gly Glu Arg Leu Ala Lys Gln Lys Ile Glu
  188                380             385                390
  190  Asp His Leu Leu Ser Ser Gly Lys Phe Met Tyr Leu Glu Gly Asn
  191                395             400                405
W--> 193  Ala Asp Ser Ala Xaa Ser
  194                410
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VERIFICATION SUMMARY
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L:107 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:2
L:193 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2